

Fig. 1



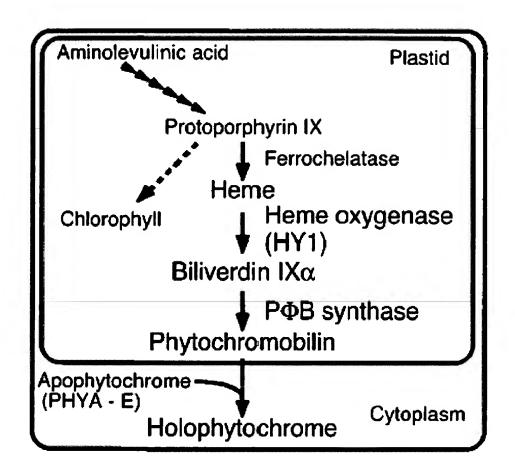


Fig. 2



qaatteeeeacgteaacgtgaetgtgeatteeacgtggeggatgtgggeeetatagt	egg ou
accatgactoggacggatgttgaaattcattgtcgttgccaattgcgtttgtctcac	tga 120
aactgtgaaaattttatctcttttatagataaAGAATCTTGCTTTTTTCAGTTTTCA	GTA 180
TGAAGAAGAATTGAAGAGAGTGTCCGAGGAAGGAGCCTTTGGTTTCAGTTTGTGAG	TCT 240
TGTTGTAATGGCTTTATCAATGGAGTTTTGGGTTTTCAATTGGGTCATGCTTCAAGGC	ACC 300
MALSMEFGFSIGSCFKA	P
AAACCCACCTGTTCTAATCTCTGCAAGCCCTAATAAGATCAATTTCACGTTGAGAAG N P P V L I S A S P N K I N F T L R R	GAG 360 R
AAAGAAAAGATTCTTACTTAGAGTCTCTGCTGTGTCGTATAAGGAATTCGCAGAGTC	TGC 420
by2-106 *****	
K K R F L L R V S A V S Y K E F A E S	A
TTTAGAAGAAACCAGGAAAAGGATCGTTCTTGAACCTTCACATCTCCAGgtatatgc L E E T R K R I V L E P S H L Q	aat 480
tacatttcgttagtgtagtgggaggattatatttctcattgtttcttgctgtgaatt	ttg 540
ggtaaattgatttgagttgtcattaggaaccaaacaaataactttactgttatagac	tgc 600
ttatataagtaaaagttcagattttgtttttctaatcacgaaactgtttcagGAAAA	GTA 660
E K	Y
TAGTAGCATGACAGGACTAGATGGTAAGACCGAACTTCAAATGCTTGCT	TTC 720
S S M T G L D G K T E L Q M L A F K S	S
AAAGATTAGACTCTTGAGGAGTATGGCAATAGAGAATGAGACAATGCAGgtttaact	tca 780
KIRLLRSMAIENETHQ	
gcagtacaaactgattgctttagtcccatttccttactttcaattgattg	gta 840
-	TAT 900
tettegettagGTCTTTGACTTTGCGGGTTTCATGGAGCCTGAGTATGATACTCCCA by2-1,by2-104 T	TAT 900
V F D F A G F M E P E Y D T P I	F
TCTGTGCTAACTTTTCACATCTACCAACGTTAACATAGTTGTATTgtaagttatct	tct 960
CANFFTSTNVNIVVL	
${\tt agttatgctggagttatcaggtctgtattgtccaaactgatgttcaatattttactg}$	tat 1020



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Fig. 3B cont'd.





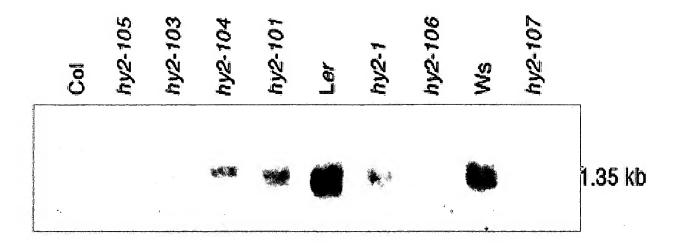


Fig. 4A

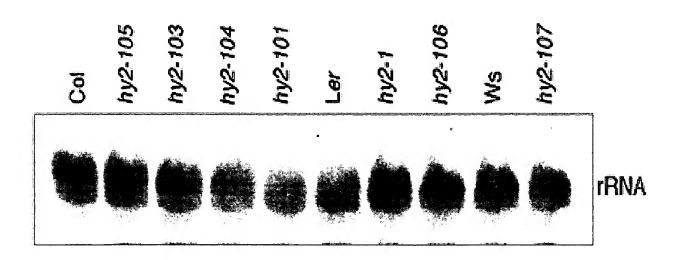


Fig. 4B



		費	20	* 40
HY2 ARATH	: Malsmefg	FSIGSCFKAP	NPPVLISASPI	KINFTLRRRKK
YCPŽ SYNPY				
YHP2 PROMA				
YHP3 PROMA		-		MIIKRDNS
YCP3 SYNPY	1			MTNQRFKS
SLROI16	:			-MAVTDLSLTN
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			PEPEGLEECRS	
			evengmserfs	
			PVSHDFLSKES	econ.
			PVPDRFLQRED	
			QUPEDLGYVEG	
SS WHE THUE W	er X.Amumumum	b Sucher	K Keernage ee	WHESE . SA
		da	•	
	T	100	*	120
HY2 ARATH	: TEL	QMLAFKS SKI	RLERSMATEN -	ETMOVEDFAGE
YCPZ SYNPY				d slov fnsvay
YHP2 PROMA	:TVI	KSWLWDVPGE	RRWRVIEMDAG	DKLQVLHSVAX
YHP3 PROMA	· BUDUUUUM	TOWARKERT	COVERN CHRCE	TO CHEST OF THE
YCP3 SYNPY	SKSIPVTT	ATWACKTEKE	ROVRAACVSAC	SAASVLMEVIN
SLROT16	: -KIVI	ENRCYQTPQE	RKMHLELAKVO	SAASVLAFVIN KGLDILECVMF
	h		4 E 6	6
*	140		60	*
ME PEYDTELF	CAMPFISTNVI	AIVVIDENP	LHQLTDQTDYQ	DKYN : 165
ED AN A DH B T W	GVDLLWFGAR	OKLVAVLDFOP	LVQDKDYL	DRY 3 : 115
PAYTNDKELL	GIDILWFGLKI	RKLVAVLDFOP	LVQ DRD YL LVQ EERYF ALK L DN I HT ALK T DE V HT	CRYK : 119
GLNDXDLFFF	GADFUTLPNG	Hu la ld 10 p	alkldniht	ENVWP: 137
PKSTYGLEFF	GGDLVTFPAG.	Hi laideo P	AIKTDEVHT	THV D : 137
RESTRETE	CCULVAGPGG.	-VSAAFADLS	TQSDRQLP	$AA \underline{Y} \underline{Q} K : 135$
p y P	g 1	1D P		

Fig. 5



IK OF,		1122	
HY2_ARATH : YCP2_SYNPY : YHP2_PROMA : YHP3_PROMA : YCP3_SYNPY : SLR0116 :	GLKEINQE DIQIKNE RIIPLHDH	Yaetfewggklt Fpdlngeetmrs Fydfnsoktmki Wosllesggeip Wrdoleyggpip	00 GESIKFES PLVMMTR- FDPNQYFSSWLLSCR- YDSNKYES PWVLLYN- KEAEPYFSTGFLMSRL EEAQPFFSTGFLMTRLEIFSEYCLFIR- FS 6 I
GGAEQADL GSFDDLQC PLSKESDNIISE PLGEEGDELIOS	ALFSAFLEYYQA SLPKAFSAFLKA SLAKILDEFLHA ILRPAFGEYLSL IVRPAFNDYLDL	40 LEMTIQVREEME YWDLHDNAKSIPS YWOVDNNNSREYI YIELLHIAKPIKK YLELAASAERVID HCHQSIVAEPISE	TIPPEEVKNL : 193 KIIPSKYEOL : 197 ER-ALKTLEG : 219 ER-SEVLLOG : 219
HY2_ARATH YCP2_SYNPY: YHP2_PROMA: YHP3_PROMA: YCP3_SYNPY: SLR0116:	ODKYDIYSAERI HINYDIYSAERI OKAYINYRSTKI ORKYTDYRAEKI OIHYGOOOOKNI	PAHGLETSHEGK PAHGLEKSYPGQ PARANECREYGK PARGMETREHGS	# 300 AKAKELLRDFLENGVD DESNRELHEFLEPASS THADQEVREFLEPHSH EWTEDYIHKVLENI EWTEAYIHTVLEDL AVAERYMSQVLEDVIQ W 6 LF
SHK			340 WDLTGQFIG : 329 : 236 : 241 : 257

Fig. 5 cont'd.



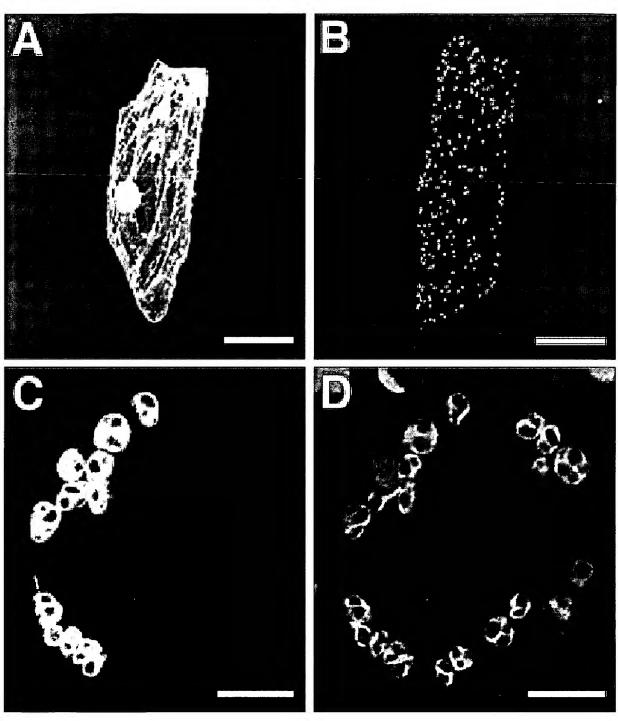


Fig. 6



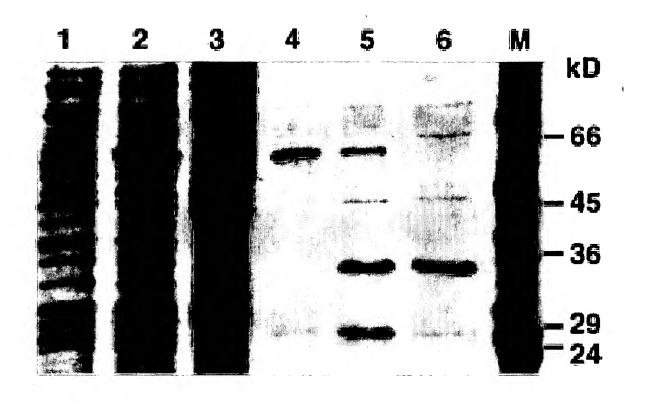
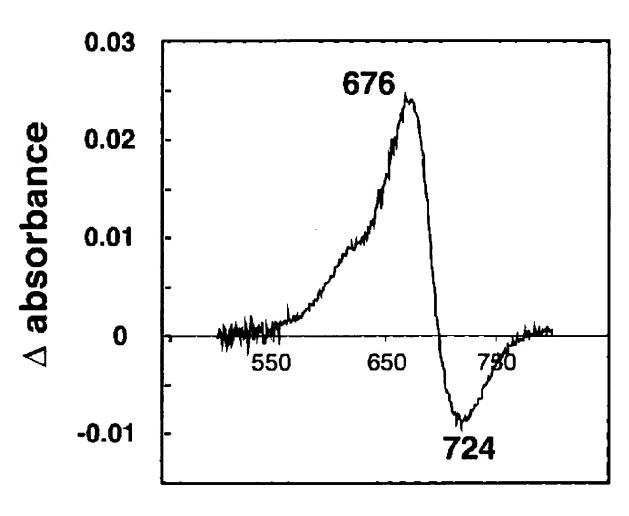


Fig. 7





Wavelength (nm)

Fig. 8



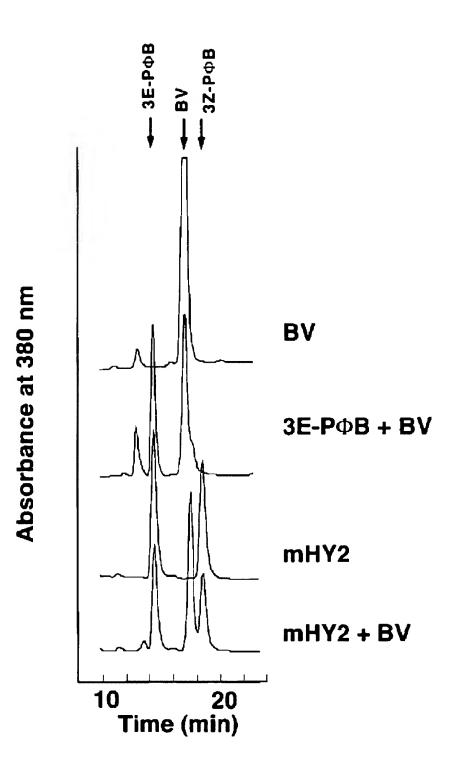


Fig. 9



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20
PCVA ANASP
PcyA_NOSPU
PcyA_SYNY3
PcyA_SYN81
PcyA_PROME
PebA_SYNPY
PebA_SYN81
Peba PROMA
PebA PROME
Peba_NOSPU
PebB_SYMPY
PebB_SYN81
PebB_PROMA
PebB_PROME
PebB NOSPU
HY2 ARATH
                          --- MALSMEFGFSIGSCFKAPN-PPVLISA
RCCR_ARATH
               MAMIFONTLY SSSSPSYLSPLTSKPSRFSKNLRPRAQFOS
RCCR_HORVU
                60
                                      80
------MSLTSIPSLREQQHP∭TRQLADOMEEVWHQHLD∭S@YH∭PAEL
                                                         43
-----MSFTSMPSLREQQHPLTRQLADOLEAAWHQHLDESEYHLPDEL
                                                         43
-- MAVTDLSLTNSSLMPTLNPMIQQLALATAASWQS-LPEKEYQEPEDL
                                                         46
-----MQSPPSESSSTVAPMIPSLAETURGAWIGLPEKKELDADSDF
                                                         42
----LNLLSKSLTKTKLIDPLILTLLQNIKVQRSKLNDENČIEDDPKL
                                                         44
                   --- MFDSFLNE HSDOTK-RGGSRLPDPEGL
                                                         27
                    ---MFDPFLEELQTGIQA-RGGISVEVPAGL
                                                         27
  -----KNKLNL Q DLH NNLKRENIS - HG GKRI ENENGM
                                                         31
                     -MFESLKNFVKTNEE---DEDGKEEEISK
                                                         25
IN ET CMIAITY FHAR VN KSCSMYKPFLE FLEKEMFQKFD QSR V PPGL
                                                         64
---MTNQRFKSTDPVNIEGWSWQPFLEDAIKREEG-LNEERYPWPDRF
---MSIDLRASSLDPVQIPGWRWQPFLDEASAA@KP-FNPS@YPLAETF
                                                         45
  --miikrdmslskidlrdwent pff ndev dkesv-feeely p<mark>w</mark>shdf
                                                         44
   - - - - - MLIQNTIFY ŠQEWRWAKFIK FEIŠQEDN - YHČVĒHK<mark>I</mark>AS DF
                                                         40
  ------MNSERSDVT YQPFLDYAI AYMRSRLDEEEY PIPTGP
                                                         37
KINFTLRRRKKRFLLRVSAVSYKEFAESALEETRKR-IVEEESHLOEKY
                                                         77
HDDHLRRKFMEFPYVSPTRKQLMVDLMSTVENRLIQS--QLLLECNLPPDV
                                                         90
```

Fig. 10



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120
                                   100
                          GYVEGRLEGEK-----LTEENRCMOTPOFEKMHLELAKVE
 PCVA ANASP
                          GYVEGRLEGEK-----LTEENRCKOTPOFRKMHLELANIG
 PcyA_NOSPU
 PcyA_SYNY3
                          GYVEGRLEGEK-----LVIENRCYQTPQFRKMHLELAKVE
                          SSIEGOLEGDD-----LLERNELLCCRGVEKEHLELARLE
 PcyA_SYN81
                          SNIISNEEGKE----LYTTENEFTKAKGFTKEHIEVAEFS
 PcyA_PROME
                          EECRSSKSS----SVEOSWLWDVPGFERWRVTRLDAE
 PebA_SYNPY
                          ehn q sq k gs-----stijq swlig v pg p rrwrvtrldag
 Peba SYN61
                          SERFSHKQD----TVIKSWLWDVPGFRWRVTRMDAG
 PebA PROMA
                          BFKEHHNKD----SKYIIKNWIEESQQYRKWRITKLDG
 Peba PROME
                          EFKVSDRGR-----NPATERSWCWQSQBLEKERYTYEDA
 PebA_NOSPU
                          LOREDOTGSKSK-SIPVTTATWACKTEKFROMRAACWSAE
 PebB_SYNPY
                          LOKEGSTGSKAK - PVPVTTATWACSTDKLEDVRCACWEA
 PebB_SYN81
                          LSKE SITGSRRN - PVHVTTLTWAAKFEKIROMRLACIKGE
 PebB_PROMA
 PebB PROME
                          Sykessygskks-kkninnftwgathokrinfaravcins
                          ESNS AVVGKGKN - QE EVVTTSY A BOTAKL BOTRA AH MOGE
 PebB_NOSPU
                          SSMTGLDG-----KTELOMLARKSSKIRLLRSMALEN-
 HY2_ARATH
                         RNFN NPNGSAEASLHIRSGDKSSPIDFVIGSWIHCKIPT
 RCCR_ARATH :
                                                                     -MDFNLQSSLHCKMPNG
 RCCR_HORVU :
                                           160
                                                                             180
NMEDIALC VMFPRPEYDEPMESCOLVGGR-GQISAAIADESPVHL---DRTL
NMEDIALC VMFPRPQYNEPMESCOLVGGR-GQISAAIADESPVHL---DRTL
KGUDIALC VMFPRPQYNEPMESCOLVGGR-GQISAAIADESPVQL---ERTL
KGUDIALC VMFPRPLYGEPLFGCDZVAGP-GGVSAAIADESPVQS---DRQL
RGDDIALC VMFPDPREDEPMESCOLVAGP-AGVSAAIVDESPV----SGTL
KSLKILLCVFFPDPKYDIPMESMOLVKVN-ELVSAAIVDESPSSK---NQNL
DSLOVFNSVAYPDYNYDHPEMGVOLLWFGARQKLVAVLDFQPEVQ---DKDY
                                                                                               126
                                                                                               126
                                                                                            : 129
                                                                                               123
DSDOVENSVAYEDFOLDHEEMGVOLLWEGARQKLVAVLDEQELVQ---DKDY
DKLDVENSVAYEAYTNDKELGIDELWEGLKEKLVAVLDEQELVQ---DKDY
DKLDVENTVAYENEKSEFEDLGADTLWEGTSQKLLAIFDYQELIQ---EKKY
ESAQIENSVVYESHNYDLELGIDFLSFG-KVKNLIVLDEQELFQ---DEDY
SAASVINEVINEKSTYGGEFEGGDIVTEP--AGHLLALDLQEAIK--TDEVH
MAASVINEVINESCREDLEFEGADIVTLE--NGHLLALDLQEAUK--LDNIH
ESHSVENLIHELNDYDEEFEGADFVTLE--NGHLLALDLQEALK--LDNIH
                                                                                               113
                                                                                            : 109
                                                                                              132
PNYSVENFLIIEKT SYNTEFLGUDFUSLE--TSHLLVLDFQFSLK--VENQF
NSEDVENFVIE PHLNYDE PFEGA DLVTLE--GGHLIALDMOPEFR--DOSAY
ETMOVEDFAGEMEPEYDT PIECA NFFTST--NVNIVVLDENSEHQLIDQTDY
VSINITS I SGELNS STKAPNEVVELIOSS-SKSLVLILDEPHRKDLVLNPDY
-AIDITSLFINLNASTDAPHEIMEFLOGS-PTSMVVLLDELPRKDLALHPEY
p g I 4 D P
                                                                                            : 124
                                                                                            : 159
                                                                                              1.81
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Fig. 10 cont'd.

220





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PcyA_ANAS1	₽ :		YNSA												ша .uz.			
PcyA_NOSPI	J ;	PES	YTTA	ΑQ	I PV	7	-[r]	nfs	QP	RE.	L P	W	GN	I -		- 8	38 C	F
PcyA_SYNY	3 :	PAA	YQX S	ΑE	DG Q)	-P]	EFE	QQ	RE.	LΡ	ΡW	GE	I -			78	
PcyA_SYNB:	l. i	PSG	TETA	AG	TP 9		_P;	AFF	VQS	RD	r þ	GW	GT	T -		_	F'S E	
PCYA_PROME	I 1	K	X DH L	SH	D K		-S1	VFK	SK	RE	ΙP	IW	GN	<u> </u>	-	- [75 F	N
PebA_SYNP:	<i>t</i> :	LOR	YFSG	KΞ	I N Q	RFE	DL	NĢE	ET	MR	ŠF	P	NQ	¥ -			75 S	
PebA_SYN8:	L s	LDR	HFDG	ΚD	LNA	RFF	'DL	NGE	ET	MR	SF	P	NQ	¥ -			75 S	
PebA_PROMA	4 :	FCR	YYKD	QI	LKN	RFV	DF!	NSÇ	KT	MK	ΙY	19	NK	¥ -	-	يت ا	75	W
PebA_PROME	3 :	LOK	YCSS	DF	KN	OY S	VF	DNE	IKM	ΚN	ΙY	79	KK	¥ -		-	78	[1]
PebA_NOSPU	J :		YIAP														rs k	
PebB_SYNP:	Č :		ŴWDR													-	?'S	G
FebB_SYN8:			VWER													- 2	r'S	P.
PebB_PROMA			VWPR													-	75	G
PebB_PROME			LLEQ												ates ates		75	
PebB_NOSPI	J :	QA K	YTEP	LP	JFH	AHC	QHI	LSW	ig g	DF:	PE	A	QP	3-			78	623
HY2_ARATH	‡		YYNK														7S	
RCCR_ARATI		TKE	YYQD	TAL	DS H	RQS	LL	KLE	EV	NP	YV	SP	SL	٧.	RS	A,	75 🛭	T
RCCR_HORVI	Ĵ :	IEK	Y YE D'	TEV	DK Q	RKI	IE(QLЕ	Αŷ	RP	ΥL	SP	SL	V.	RS	A	ng E	7
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'CIPVRP		- SSP - GSP	ee eam ee eam	IFLG IFLS	RVE	EFI	D.	HC Q HC M	QA I	AS		HP	vsv	/EQ	V		19 19	9
'CIFURP		- SSP - GSP - SNV	ee eam ee eam te eer	FLS	RVE	REFI MDF1	QI DI DI	HC Q HC M HC H	QA I QS I	AS VA		HP EP	VSV LSE	/E(V(T(4 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -	19 19 20	9 2
CLFURP CLFIRP IVCFIRP		- SSP - GSP - SNV - DGA	ee ean ee ean te eer ee evi	# IFLO IFLS IFVQ	RVI RVI	REFI VDFI SEVI		HCQ HCM HCH LRT	QA I QS I AV L	AS VA QT	 AC	HP EP EP	VSV LSE ATA	EAC NAS	V(T(T(4P 2F 2F 2F 5	19 19 20	9 2 8
'CLFIRP 'CLFIRP IVCFIRP IVFFASL		- SSP - GSP - SNV - DGA - KNE	EE EAM EE EAM TE EER EE EVI SE KNA	IFLG IFLS IFVC IFRS	RVE RVI RVI	ON A I		HCQ HCM HCH LRT LIQ	QAI QSI AVL LSQ	AS VA QT ST	 AC	HP EP EP SP	VSV LSE ATA DSE	EAC AAS YE	V T T T	4 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -	19 19 20 19	9 2 8 8
CIFVRP CLFIRP IVCPIRP IVFPASL ILFCRG		- SSP - GSP - SNV - DGA - KNE - GAE	ee eam ee eam te eer ee evl se kna Qa dls	IF LG IF LS IF VC IF CK	RVE RVE RVE ELVE LAFS	REFI ONY I SAFI	OD OT SX	HCQ HCM HCH LRT LIQ WD	QAI QSI AVL LSQ LH D	AS VA QT ST NA	 AC	HP EP EP SP KS	VSV LSE ATA DSE IPS	EAC AAS YE STI	V T F EI	4 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -	19 19 20 19 19	9 2 8 8 6
CIFURP ICLFIRP IVEPASL ILLFCRG ILLFCRG		- SSP - GSP - SNV - DGA - KNE - GAE - GSE	EE EAM EE EAM TE EER EE EVL SE KNA QA DLS EA DRS	FLS FVC FRS FCK FCK FCK FCK FCK FCK	RVE RVE RVE LVE LAFS LAFS	PEFI /DFI EEVI ONYI SAFI SAFI	NA CLOKK NA CLOKK	HCQ HCM HCH LRT LIQ MND MNG	QAI QSI AVL LSQ LHC LHC	AS VA QT ST NA EA	AC	HP EP EP SP KS SK	VSV LSE ATA DSE EPS	VEQ ZAQ XAS SYE STI	Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y	4 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -	19 19 20 19	9 2 8 8 6
CIFVRP CLFIRP IVCPIRP IVFPASL ILFCRG		- SSP - GSP - SNV - DGA - KNE - GAE - GSE - SPD	EE EAM EE EAM TE EER EE EVU SE KNA QA DLS EA DRS	IFLO IFLS IFVO IFRS IFCH IPPR	RVE RVE RVE LVE LAFS LAFS	PEFI VDFI SEVI SAFI SAFI JEFI	NA N	HCQ HCM HCH LRT LIQ WD WG	QAI QSI AVL LSQ LHC LHC VDN	AS VA QT ST NA EA NN	AC	HP EP SP KS KS SR	VSV LSE ATA DSI IPS EPS EYI	VE(EA(VAS OYE STI SSI KI	Y T T T T T T T T T T T T T T T T T T T	47 27 27 27 20 20	19 19 20 19 18 18	9 2 8 6 6 0
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Fig. 10 cont'd.





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PcyA_SYNB1		IRRYE-							
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FIFPHSHLTAD-									: 241
IFILETINHN PLK -	-			**** *** *** ***					: 236
FLFEDAVPLAVS	AS.	K R							: 280
MULDI									: 257
WLFDLEDAA									: 262
VLFNI									
VLFSTNKVL									
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Fig. 10 cont'd.



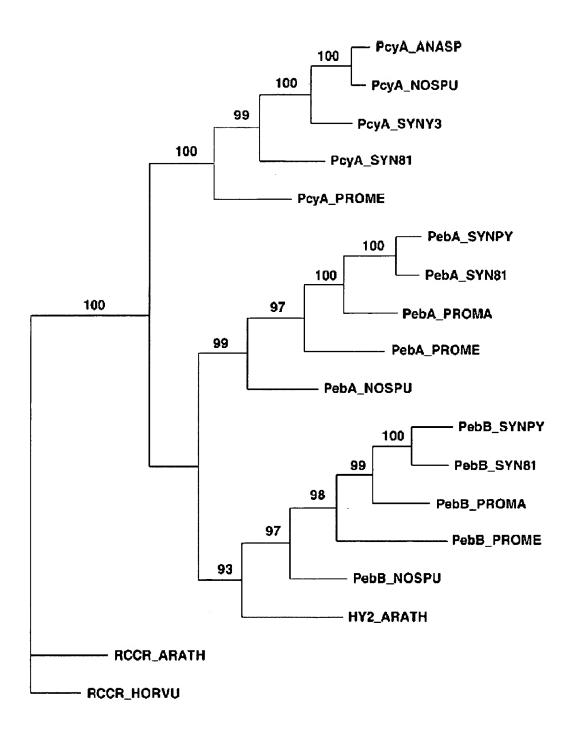


Fig. 11





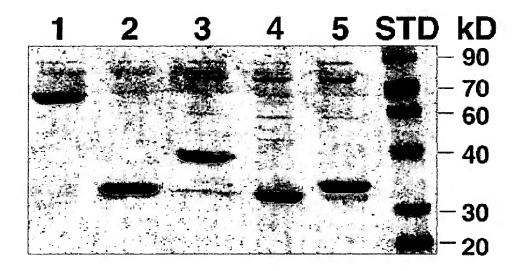


Fig. 12





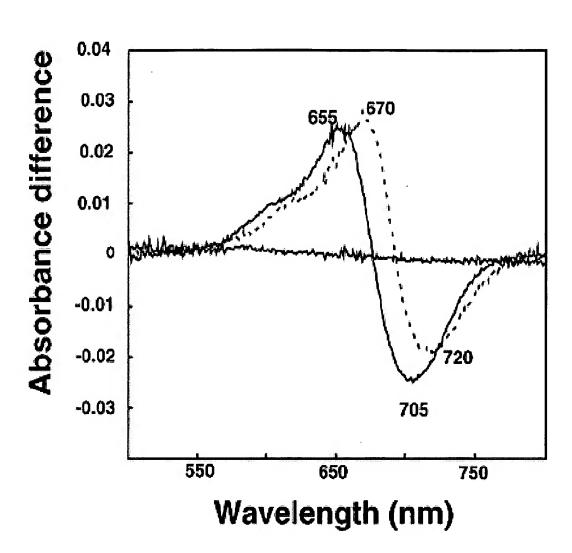


Fig. 13A





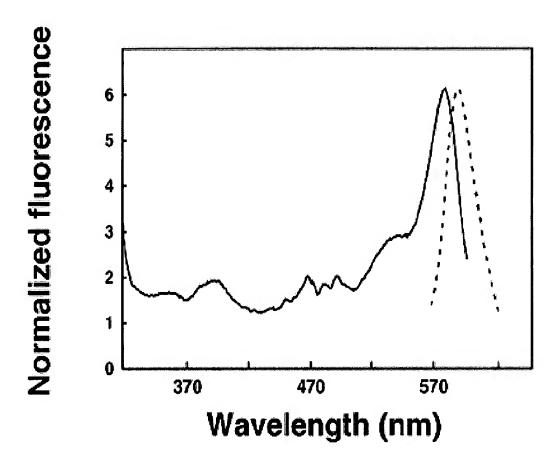


Fig. 13B







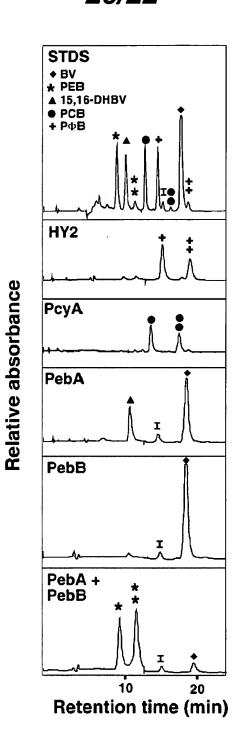


Fig. 14





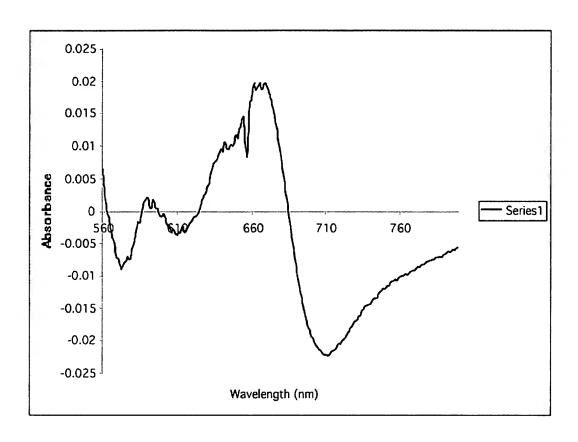


Fig. 15



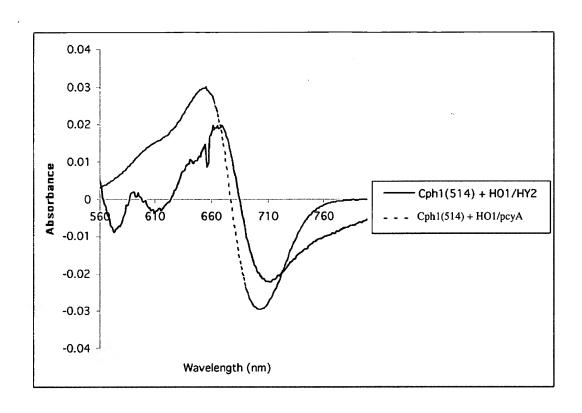


Fig. 16